IN THE SPECIFICATION:

Please amend the specification as follows:

At page 17, please revise the paragraph starting at line 13 as follows:

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al., Nuc. Acids Res.,* 25:3389-402 (1977) and Altschul *et al., J Mol. Biol.,* 215:403-10 (1990), respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http:..www.ncbi.nlm.nih.gov/)~~. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al., Nuc. Acids Res.,* 25:3389-402 (1977) and Altschule *et al., J Mol. Biol.,* 215:403-10 (1990)). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in

each direction are halted when: the cumulative alignment score falls off by the quantity X from is maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=4 and a comparison for both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *PNAS*, 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands.

At page 37, paragraph starting at line 19, please amend as follows:

Paradigms to design degenerate primer pairs are well known in the art. For example, COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) strategy computer program is accessible as ~~http://blocks.fhcrc.org/codehop.html~~, and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known taste receptor ligand-binding regions (*see, e.g.,* Rose, *Nucleic Acids Res.,* 26:1628-35 (1998); Singh, *Biotechniques*, 24:318-19 (1998)).

IN THE CLAIMS:

The following listing of claims replaces all prior versions and listings of claims in the present application.

Listing of Claims:

Kindly delete claims 1-157 and substitute the following:

158. (New) An isolated nucleic acid molecule encoding a bitter taste receptor selected from the group consisting of

(i) an isolated nucleic acid sequence having the nucleic acid sequence contained in SEQ ID NO:7;

(ii) a nucleic acid sequence that encodes the bitter taste polypeptide contained in SEQ ID NO:8; and

(iii) an isolated DNA sequence that hybridizes under stringent hybridization conditions to the nucleic acid sequence contained in SEQ ID NO:7 wherein stringent hybridization conditions are hybridization in 5 x SSC, 1% SDS, incubation at 65°C and wash in 0.2 x 55C and 0.1% SDS at 65°C, wherein said hybridization and wash steps are each effected for at least 1 minute.

159. (New) An isolated nucleic acid molecule encoding a bitter taste receptor polypeptide which polypeptide comprises at least 95% identity to the taste receptor polypeptide contained in SEQ ID NO:8.

160. (New) An isolated nucleic acid molecule which consists of the nucleic acid sequence contained in SEQ ID NO:7.

161. (New) An isolated nucleic acid molecule which encodes the receptor polypeptide contained in SEQ ID NO:8 which is operably linked to a promoter that regulates the expression of said polypeptide.

162. (New) The isolated nucleic acid molecule of claim 161 wherein said promoter is constitutive.

163. (New) The isolated nucleic acid molecule of claim 161 wherein said promoter is regulatable.

164. (New) An isolated nucleic acid sequence according to claim 159 which encodes a bitter taste receptor having at least 96% sequence identity to the polypeptide contained in SEQ ID NO:8.

165. (New) An isolated nucleic acid sequence according to claim 159 which encodes a bitter taste receptor having at least 97% sequence identity to the polypeptide contained in SEQ ID NO:8.

166. (New) An isolated nucleic acid sequence according to claim 159 which encodes a bitter taste receptor having at least 98% sequence identity to the polypeptide contained in SEQ ID NO:8.

167. (New) An isolated nucleic acid sequence according to claim 159 which encodes a bitter taste receptor having at least 99% sequence identity to the polypeptide contained in SEQ ID NO:8.

168. (New) An isolated nucleic acid molecule according to claim 159 which is operably linked to a promoter that regulates the transcription thereof.

169. (New) The isolated nucleic acid molecule of claim 168 wherein said promoter is constitutive.

170. (New) The isolated nucleic acid molecule of claim 168 wherein said promoter is regulatable.

171. (New) An isolated nucleic acid sequence according to claim 158 attached to a nucleic acid sequence encoding a chaperone protein.

172. (New) An expression vector containing an isolated nucleic acid molecule according to claim 158.

173. (New) An expression vector containing an isolated nucleic acid molecule according to claim 159.

174. (New) A cell which is transfected or transformed with an isolated nucleic acid molecule according to claim 158.

175. (New) A cell which is transfected or transformed with an isolated nucleic acid molecule according to claim 159.

176. (New) The cell of claim 174 which is selected from a mammalian, insect, amphibian, yeast, and bacterial cell.

177. (New) The cell of claim 174 which is a mammalian cell.

178. (New) The cell of claim 174 which additionally expresses a G protein.

179. (New) The cell of claim 178 wherein said G protein is $G_{\alpha 15}$.

180. (New) The cell of claim 179 which is an HEK-293 cell.

181. (New) The cell of claim 175 which is selected from a mammalian, amphibian, yeast, insect and bacterial cell.

182. (New) The cell of claim 181 which is a mammalian cell.

183. (New) The cell of claim 175 which further expresses a G protein.

184. (New) The cell of claim 183 wherein said G protein is $G_{\alpha 15}$.

185. (New) The cell of claim 184 which is an HEK-293 cell.